

SEQUENCE LISTING

<110> Perrin, Marilyn H.
Chen, Ruoping
Lewis, Kathy A.
Vale Jr., Wylie W.
Donaldson, Cynthia J.
Sawchenko, Paul

<120> Cloning and Recombinant Production of
CRF Receptor(s)

<130> Salk1748

<150> US 08/374,009
<151> 1995-01-17

<150> US 08/353,537
<151> 1994-12-09

<150> PCT/US94/05908
<151> 1993-05-25

<150> US 08/110,286
<151> 1993-08-23

<150> US 08/079,320
<151> 1993-06-18

<160> 15

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<213> Homo sapiens

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/note= "This sequence is encoded by clone
"CRF-R1"."

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Met Gly Gly His Pro Gln Leu Arg Leu Val

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aag gcc ctt ctc ctt ctg ggg ctg aac ccc gtc tct gcc tcc ctc cag 159
 Lys Ala Leu Leu Leu Leu Gly Leu Asn Pro Val Ser Ala Ser Leu Gln

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gac cag cac tgc gag agc ctg tcc ctg gcc agc aac atc tca gga ctg 207
 Asp Gln His Cys Glu Ser Leu Ser Leu Ala Ser Asn Ile Ser Gly Leu

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cag tgc aac gca tcc gtg gac ctc att ggc acc tgc tgg ccc cgc agc 255
 Gln Cys Asn Ala Ser Val Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser

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cct gcg ggg cag cta gtg gtt cgg ccc tgc cct gcc ttt ttc tat ggt 303
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 Val Arg Tyr Asn Thr Thr Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn

75 80 85 90

ggc agc tgg gcc gcc cgc gtg aat tac tcc gag tgc cag gag atc ctc 399
 Gly Ser Trp Ala Ala Arg Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu

95 100 105

aat gag gag aaa aaa agc aag gtg cac tac cat gtc gca gtc atc atc 447
 Asn Glu Glu Lys Lys Ser Lys Val His Tyr His Val Ala Val Ile Ile

110 115 120

aac tac ctg ggc cac tgt atc tcc ctg gtg gcc ctc ctg gtg gcc ttt 495
 Asn Tyr Leu Gly His Cys Ile Ser Leu Val Ala Leu Leu Val Ala Phe

125 130 135

gtc ctc ttt ctg cgg ctc agg agc atc cgg tgc ctg cga aac atc atc 543
 Val Leu Phe Leu Arg Leu Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile

140 145 150

cac tgg aac ctc atc tcc gcc ttc atc ctg cgc aac gcc acc tgg ttc 591
 His Trp Asn Leu Ile Ser Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe

155 160 165 170
 gtg gtc cag cta acc atg agc ccc gag gtc cac cag agc aac gtg ggc 639
 Val Val Gln Leu Thr Met Ser Pro Glu Val His Gln Ser Asn Val Gly
 175 180 185
 tgg tgc agg ttg gtg aca gcc gcc tac aac tac ttc cat gtg acc aac 687
 Trp Cys Arg Leu Val Thr Ala Ala Tyr Asn Tyr Phe His Val Thr Asn
 190 195 200
 ttc ttc tgg atg ttc ggc gag ggc tgc tac ctg cac aca gcc atc gtg 735
 Phe Phe Trp Met Phe Gly Glu Gly Cys Tyr Leu His Thr Ala Ile Val
 205 210 215
 ctc acc tac tcc act gac cgg ctg cgc aaa tgg atg ttc atc tgc att 783
 Leu Thr Tyr Ser Thr Asp Arg Leu Arg Lys Trp Met Phe Ile Cys Ile
 220 225 230
 ggc tgg ggt gtg ccc ttc ccc atc att gtg gcc tgg gcc att ggg aag 831
 Gly Trp Gly Val Pro Phe Pro Ile Ile Val Ala Trp Ala Ile Gly Lys
 235 240 245 250
 ctg tac tac gac aat gag aag tgc tgg ttt ggc aaa agg cct ggg gtg 879
 Leu Tyr Tyr Asp Asn Glu Lys Cys Trp Phe Gly Lys Arg Pro Gly Val
 255 260 265
 tac acc gac tac atc tac cag ggc ccc atg atc ctg gtc ctg atc 927
 Tyr Thr Asp Tyr Ile Tyr Gln Gly Pro Met Ile Leu Val Leu Leu Ile
 270 275 280
 aat ttc atc ttc ctt ttc aac atc gtc cgc atc ctc atg acc aag ctc 975
 Asn Phe Ile Phe Leu Phe Asn Ile Val Arg Ile Leu Met Thr Lys Leu
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 Arg Ala Ser Thr Thr Ser Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys
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 Ala Thr Leu Val Leu Leu Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe
 315 320 325 330
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 Phe Val Asn Pro Gly Glu Asp Glu Val Ser Arg Val Val Phe Ile Tyr
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 Tyr Cys Phe Leu Asn Ser Glu Val Arg Ser Ala Ile Arg Lys Arg Trp
 365 370 375

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 His Arg Trp Gln Asp Lys His Ser Ile Arg Ala Arg Val Ala Arg Ala
 380 385 390

atg tcc atc ccc acc tcc cca acc cgt gtc agc ttt cac agc atc aag 1311
 Met Ser Ile Pro Thr Ser Pro Thr Arg Val Ser Phe His Ser Ile Lys
 395 400 405 410

cag tcc aca gca gtc tgagctggca ggcatggag cagccccaa agagctgtgg 1366
 Gln Ser Thr Ala Val
 415

ctgggggggat gacggccagg ctccctgacc accctgcctg tggaggtagac ctgttaggtc 1426
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<212> PRT

<213> Homo sapiens

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 35 40 45
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 50 55 60
 Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly Val Arg Tyr Asn Thr Thr
 65 70 75 80
 Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn Gly Ser Trp Ala Ala Arg
 85 90 95
 Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu Asn Glu Glu Lys Lys Ser
 100 105 110

Lys Val His Tyr His Val Ala Val Ile Ile Asn Tyr Leu Gly His Cys
 115 120 125
 Ile Ser Leu Val Ala Leu Leu Val Ala Phe Val Leu Phe Leu Arg Leu
 130 135 140
 Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile His Trp Asn Leu Ile Ser
 145 150 155 160
 Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe Val Val Gln Leu Thr Met
 165 170 175
 Ser Pro Glu Val His Gln Ser Asn Val Gly Trp Cys Arg Leu Val Thr
 180 185 190
 Ala Ala Tyr Asn Tyr Phe His Val Thr Asn Phe Phe Trp Met Phe Gly
 195 200 205
 Glu Gly Cys Tyr Leu His Thr Ala Ile Val Leu Thr Tyr Ser Thr Asp
 210 215 220
 Arg Leu Arg Lys Trp Met Phe Ile Cys Ile Gly Trp Gly Val Pro Phe
 225 230 235 240
 Pro Ile Ile Val Ala Trp Ala Ile Gly Lys Leu Tyr Tyr Asp Asn Glu
 245 250 255
 Lys Cys Trp Phe Gly Lys Arg Pro Gly Val Tyr Thr Asp Tyr Ile Tyr
 260 265 270
 Gln Gly Pro Met Ile Leu Val Leu Leu Ile Asn Phe Ile Phe Leu Phe
 275 280 285
 Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser
 290 295 300
 Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu
 305 310 315 320
 Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu
 325 330 335
 Asp Glu Val Ser Arg Val Val Phe Ile Tyr Phe Asn Ser Phe Leu Glu
 340 345 350
 Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr Cys Phe Leu Asn Ser
 355 360 365
 Glu Val Arg Ser Ala Ile Arg Lys Arg Trp His Arg Trp Gln Asp Lys
 370 375 380
 His Ser Ile Arg Ala Arg Val Ala Arg Ala Met Ser Ile Pro Thr Ser
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 Pro Thr Arg Val Ser Phe His Ser Ile Lys Gln Ser Thr Ala Val
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Met Gly Arg Arg Pro Gln Leu Arg Leu Val Lys
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gcc ctt ctc ctt ctg ggg ctg aac cct gtg tcc acc tcc ctt cag gat 160
Ala Leu Leu Leu Leu Gly Leu Asn Pro Val Ser Thr Ser Leu Gln Asp
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cag cgc tgt gag aac ctg tcc ctg acc agc aat gtt tct ggc ctg cag 208

Gln Arg Cys Glu Asn Leu Ser Leu Thr Ser Asn Val Ser Gly Leu Gln
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 Cys Asn Ala Ser Val Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser Pro
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ggc ggc cag ttg gtg gtc cga ccc tgc cct gcc ttt ttc tac ggt gtc 304
 Ala Gly Gln Leu Val Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly Val
 60 65 70 75

cgc tac aac acg aca aac aat ggc tac egg gag tgc ctg gcc aac ggc 352
 Arg Tyr Asn Thr Thr Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn Gly
 80 85 90

agc tgg gca gcc cgt gtg aat tat tct gag tgc cag gag att ctc aac 400
 Ser Trp Ala Ala Arg Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu Asn
 95 100 105

gaa gag aag aag agc aaa gta cac tac cat gtt gca gtc atc atc aac 448
 Glu Glu Lys Lys Ser Lys Val His Tyr His Val Ala Val Ile Ile Asn
 110 115 120

tac ctg ggt cac tgc atc tcc ctg gta gcc ctc ctg gtg gcc ttt gtc 496
 Tyr Leu Gly His Cys Ile Ser Leu Val Ala Leu Leu Val Ala Phe Val
 125 130 135

ctc ttc ttg egg ctc agg agc atc egg tgc ctg aga aac atc atc cac 544
 Leu Phe Leu Arg Leu Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile His
 140 145 150 155

tgg aac ctc atc tgc gct ttc atc cta cgc aac gcc acg tgg ttt gtg 592
 Trp Asn Leu Ile Ser Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe Val
 160 165 170

gtc cag ctc acc gtg agc ccc gag gtg cac cag agc aat gtg gcc tgg 640
 Val Gln Leu Thr Val Ser Pro Glu Val His Gln Ser Asn Val Ala Trp
 175 180 185

tgt agg ttg gtg aca gcc gcc tac aat tac ttc cat gta acc aac ttc 688
 Cys Arg Leu Val Thr Ala Ala Tyr Asn Tyr Phe His Val Thr Asn Phe
 190 195 200

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205 210 215
 acg tac tcc acc gac cgt ctg cgc aag tgg atg ttc gtc tgc att ggc 784
 Thr Tyr Ser Thr Asp Arg Leu Arg Lys Trp Met Phe Val Cys Ile Gly
 220 225 230 235

 tgg ggt gta cct ttc ccc atc att gtg gct tgg gcc att ggg aag ctg 832
 Trp Gly Val Pro Phe Pro Ile Ile Val Ala Trp Ala Ile Gly Lys Leu
 240 245 250

 cac tac gac aat gaa aag tgc tgg ttt ggc aaa cgt cct ggg gta tac 880
 His Tyr Asp Asn Glu Lys Cys Trp Phe Gly Lys Arg Pro Gly Val Tyr
 255 260 265

 act gac tac atc tac cag ggc ccc atg atc ctg gtc ctg ctg atc aac 928
 Thr Asp Tyr Ile Tyr Gln Gly Pro Met Ile Leu Val Leu Leu Ile Asn
 270 275 280

 ttt atc ttt ctc ttc aac att gtc cgc atc ctc atg acc aaa ctc cgg 976
 Phe Ile Phe Leu Phe Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg
 285 290 295

 gca tcc act aca tct gag acc att cag tac agg aag gct gtg aag gcc 1024
 Ala Ser Thr Thr Ser Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala
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 act ctg gtg ctc ctg ccc ctt ctg ggc atc acc tac atg ttg ttc ttc 1072
 Thr Leu Val Leu Leu Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe
 320 325 330

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 Val Asn Pro Gly Glu Asp Glu Val Ser Arg Val Val Phe Ile Tyr Phe
 335 340 345

 aac tct ttt ctg gag tcc ttt cag ggc ttc ttt gtg tct gtg ttc tac 1168
 Asn Ser Phe Leu Glu Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr
 350 355 360

 tgt ttt ctg aac agt gag gtc cgc tcc gct atc cgg aag agg tgg cgt 1216
 Cys Phe Leu Asn Ser Glu Val Arg Ser Ala Ile Arg Lys Arg Trp Arg
 365 370 375

 cgg tgg cag gac aag cac tcc atc aga gcc cga gtg gcc cga gct atg 1264
 Arg Trp Gln Asp Lys His Ser Ile Arg Ala Arg Val Ala Arg Ala Met
 380 385 390 395

tcc atc ccc acc tcc ccg acc aga gtc agc ttt cac agc atc aag cag 1312
 Ser Ile Pro Thr Ser Pro Thr Arg Val Ser Phe His Ser Ile Lys Gln
 400 405 410

tcc aca gca gtg tgagctccag gccacagagc agccccaag acctgaggcc 1364
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 35 40 45
 Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser Pro Ala Gly Gln Leu Val
 50 55 60
 Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly Val Arg Tyr Asn Thr Thr
 65 70 75 80
 Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn Gly Ser Trp Ala Ala Arg
 85 90 95
 Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu Asn Glu Glu Lys Lys Ser
 100 105 110
 Lys Val His Tyr His Val Ala Val Ile Ile Asn Tyr Leu Gly His Cys
 115 120 125
 Ile Ser Leu Val Ala Leu Leu Val Ala Phe Val Leu Phe Leu Arg Leu
 130 135 140
 Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile His Trp Asn Leu Ile Ser
 145 150 155 160
 Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe Val Val Gln Leu Thr Val
 165 170 175
 Ser Pro Glu Val His Gln Ser Asn Val Ala Trp Cys Arg Leu Val Thr
 180 185 190
 Ala Ala Tyr Asn Tyr Phe His Val Thr Asn Phe Phe Trp Met Phe Gly
 195 200 205
 Glu Gly Cys Tyr Leu His Thr Ala Ile Val Leu Thr Tyr Ser Thr Asp
 210 215 220

Arg Leu Arg Lys Trp Met Phe Val Cys Ile Gly Trp Gly Val Pro Phe
 225 230 235 240
 Pro Ile Ile Val Ala Trp Ala Ile Gly Lys Leu His Tyr Asp Asn Glu
 245 250 255
 Lys Cys Trp Phe Gly Lys Arg Pro Gly Val Tyr Thr Asp Tyr Ile Tyr
 260 265 270
 Gln Gly Pro Met Ile Leu Val Leu Leu Ile Asn Phe Ile Phe Leu Phe
 275 280 285
 Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser
 290 295 300
 Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu
 305 310 315 320
 Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu
 325 330 335
 Asp Glu Val Ser Arg Val Val Phe Ile Tyr Phe Asn Ser Phe Leu Glu
 340 345 350
 Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr Cys Phe Leu Asn Ser
 355 360 365
 Glu Val Arg Ser Ala Ile Arg Lys Arg Trp Arg Arg Trp Gln Asp Lys
 370 375 380
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 Phe Phe Trp Met Phe Val Glu Gly Cys Tyr Leu His Thr Ala Ile Val
 20 25 30

atg acg tac tcc aca gag cac ctg cgc aag tgg ctt ttc ctc ttc att 144
 Met Thr Tyr Ser Thr Glu His Leu Arg Lys Trp Leu Phe Leu Phe Ile

35 40 45
 gga tgg tgc att ccc tgc cct atc atc atc gcc tgg gca gtt ggc aaa 192
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 65 70

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 Met Thr Tyr Ser Thr Glu His Leu Arg Lys Trp Leu Phe Leu Phe Ile
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 Leu Tyr Tyr Glu Asn Glu
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 Met Gly Thr Pro Gly Ser Leu Pro Ser Ala Gln
 1 5 10

ctt ctc ctc tgc ctg ttt tcc ctg ctt cca gtg ctc cag gtg gcc caa 159
 Leu Leu Leu Cys Leu Phe Ser Leu Leu Pro Val Leu Gln Val Ala Gln

15 20 25
 cca ggc cag gca ccc cag gac cag ccc ctg tgg aca ctt ttg gag cag 207
 Pro Gly Gln Ala Pro Gln Asp Gln Pro Leu Trp Thr Leu Leu Glu Gln
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tac tgc cac agg acc aca att ggg aat ttt tca ggt ccc tac acc tac 255
 Tyr Cys His Arg Thr Thr Ile Gly Asn Phe Ser Gly Pro Tyr Thr Tyr
 45 50 55

tgc aac acg acc ttg gac cag atc ggg acc tgc tgg cca cag agc gca 303
 Cys Asn Thr Thr Leu Asp Gln Ile Gly Thr Cys Trp Pro Gln Ser Ala
 60 65 70 75

ccc gga gcc cta gta gag aga ccg tgc ccc gag tac ttc aat ggc atc 351
 Pro Gly Ala Leu Val Glu Arg Pro Cys Pro Glu Tyr Phe Asn Gly Ile
 80 85 90

aag tac aac acg acc cgg aat gcc tac aga gag tgc ctg gag aac ggg 399
 Lys Tyr Asn Thr Thr Arg Asn Ala Tyr Arg Glu Cys Leu Glu Asn Gly
 95 100 105

acc tgg gcc tca agg gtc aac tac tca cac tgc gaa ccc att ttg gat 447
 Thr Trp Ala Ser Arg Val Asn Tyr Ser His Cys Glu Pro Ile Leu Asp
 110 115 120

gac aag cag aga aag tat gac ctg cat tac cga atc gcc ctc att gtc 495
 Asp Lys Gln Arg Lys Tyr Asp Leu His Tyr Arg Ile Ala Leu Ile Val
 125 130 135

aac tac ctg ggt cac tgt gtt tcc gtg gtg gcc ctg gtg gcc gct ttc 543
 Asn Tyr Leu Gly His Cys Val Ser Val Val Ala Leu Val Ala Ala Phe
 140 145 150 155

ctg ctt ttc cta gtg ctg cgg agt atc cgc tgc ctg agg aat gtg atc 591
 Leu Leu Phe Leu Val Leu Arg Ser Ile Arg Cys Leu Arg Asn Val Ile
 160 165 170

cac tgg aac ctc atc acc acc ttc att ctg aga aac atc gcg tgg ttc 639
 His Trp Asn Leu Ile Thr Thr Phe Ile Leu Arg Asn Ile Ala Trp Phe
 175 180 185

ctg ctg caa ctc atc gac cac gaa gtg cac gag ggc aat gag gtc tgg 687
 Leu Leu Gln Leu Ile Asp His Glu Val His Glu Gly Asn Glu Val Trp
 190 195 200

tgc cgc tgc atc acc acc atc ttc aac tat ttt gtg gtc acc aac ttc 735
 Cys Arg Cys Ile Thr Thr Ile Phe Asn Tyr Phe Val Val Thr Asn Phe
 205 210 215

ttc tgg atg ttt gtg gag ggc tgc tac ctg cac acg gcc att gtc atg 783
 Phe Trp Met Phe Val Glu Gly Cys Tyr Leu His Thr Ala Ile Val Met
 220 225 230 235

acg tac tcc aca gag cac ctg cgc aag tgg ctt ttc ctc ttc att gga 831
 Thr Tyr Ser Thr Glu His Leu Arg Lys Trp Leu Phe Leu Phe Ile Gly
 240 245 250

tgg tgc att ccc tgc cct atc atc atc gcc tgg gca gtt ggc aaa ctc 879
 Trp Cys Ile Pro Cys Pro Ile Ile Ile Ala Trp Ala Val Gly Lys Leu
 255 260 265

tac tat gag aat gag cag tgc tgg ttt ggc aag gaa gct ggt gat ttg 927
 Tyr Tyr Glu Asn Glu Gln Cys Trp Phe Gly Lys Glu Ala Gly Asp Leu
 270 275 280

gtg gac tac atc tac cag ggc ccc gtc atg ctt gtg ctg ttg atc aat 975
 Val Asp Tyr Ile Tyr Gln Gly Pro Val Met Leu Val Leu Leu Ile Asn
 285 290 295

ttt gta ttt ctg ttt aac atc gtc agg atc ctg atg acg aag tta cga 1023
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gca tcc acc acg tcc gag aca atc caa tac agg aag gca gtg aag gcc 1071
 Ala Ser Thr Thr Ser Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala
 320 325 330

acg ctg gtc ctc ctc ccc ctg ttg ggc atc acc tac atg ctc ttc ttt 1119
 Thr Leu Val Leu Leu Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe
 335 340 345

gtc aat cct ggc gag gac gac ctg tcc cag att gtg ttc atc tac ttc 1167
 Val Asn Pro Gly Glu Asp Asp Leu Ser Gln Ile Val Phe Ile Tyr Phe
 350 355 360

aac tet ttc ctg cag tcc ttc cag ggt ttc ttt gtg tcc gtt ttc tac 1215
 Asn Ser Phe Leu Gln Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr
 365 370 375

tgc ttc ttc aat gga gag gtg cgc gcg gcc ctg aga aag cgg tgg cac 1263
 Cys Phe Phe Asn Gly Glu Val Arg Ala Ala Leu Arg Lys Arg Trp His
 380 385 390 395

cgc tgg cag gac cac cac gcc ctc cgg gtg cct gtg gcc cgg gcc atg 1311
 Arg Trp Gln Asp His His Ala Leu Arg Val Pro Val Ala Arg Ala Met
 400 405 410

tcc atc cct acg tgc ccc acc agg atc agc ttc cac agc atc aag cag 1359
 Ser Ile Pro Thr Ser Pro Thr Arg Ile Ser Phe His Ser Ile Lys Gln
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 35 40 45
 Thr Ile Gly Asn Phe Ser Gly Pro Tyr Thr Tyr Cys Asn Thr Thr Leu
 50 55 60
 Asp Gln Ile Gly Thr Cys Trp Pro Gln Ser Ala Pro Gly Ala Leu Val
 65 70 75 80
 Glu Arg Pro Cys Pro Glu Tyr Phe Asn Gly Ile Lys Tyr Asn Thr Thr
 85 90 95
 Arg Asn Ala Tyr Arg Glu Cys Leu Glu Asn Gly Thr Trp Ala Ser Arg
 100 105 110
 Val Asn Tyr Ser His Cys Glu Pro Ile Leu Asp Asp Lys Gln Arg Lys
 115 120 125
 Tyr Asp Leu His Tyr Arg Ile Ala Leu Ile Val Asn Tyr Leu Gly His
 130 135 140
 Cys Val Ser Val Val Ala Leu Val Ala Ala Phe Leu Leu Phe Leu Val
 145 150 155 160
 Leu Arg Ser Ile Arg Cys Leu Arg Asn Val Ile His Trp Asn Leu Ile
 165 170 175

Thr Thr Phe Ile Leu Arg Asn Ile Ala Trp Phe Leu Leu Gln Leu Ile
 180 185 190
 Asp His Glu Val His Glu Gly Asn Glu Val Trp Cys Arg Cys Ile Thr
 195 200 205
 Thr Ile Phe Asn Tyr Phe Val Val Thr Asn Phe Phe Trp Met Phe Val
 210 215 220
 Glu Gly Cys Tyr Leu His Thr Ala Ile Val Met Thr Tyr Ser Thr Glu
 225 230 235 240
 His Leu Arg Lys Trp Leu Phe Leu Phe Ile Gly Trp Cys Ile Pro Cys
 245 250 255
 Pro Ile Ile Ile Ala Trp Ala Val Gly Lys Leu Tyr Tyr Glu Asn Glu
 260 265 270
 Gln Cys Trp Phe Gly Lys Glu Ala Gly Asp Leu Val Asp Tyr Ile Tyr
 275 280 285
 Gln Gly Pro Val Met Leu Val Leu Leu Ile Asn Phe Val Phe Leu Phe
 290 295 300
 Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser
 305 310 315 320
 Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu
 325 330 335
 Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu
 340 345 350
 Asp Asp Leu Ser Gln Ile Val Phe Ile Tyr Phe Asn Ser Phe Leu Gln
 355 360 365
 Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr Cys Phe Phe Asn Gly
 370 375 380
 Glu Val Arg Ala Ala Leu Arg Lys Arg Trp His Arg Trp Gln Asp His
 385 390 395 400
 His Ala Leu Arg Val Pro Val Ala Arg Ala Met Ser Ile Pro Thr Ser
 405 410 415
 Pro Thr Arg Ile Ser Phe His Ser Ile Lys Gln Thr Ala Ala Val
 420 425 430

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> "sense" probe for CRF-RB1

<400> 11

ctgcatcacc accatcttca act

23

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> "antisense" probe for CRF-RB1

<400> 12

agccacttgc gcaggtgctc

20

<210> 13

<211> 415

<212> PRT

<213> Mus musculus

<400> 13

Met Gly Gln Arg Pro Gln Leu Arg Leu Val Lys Ala Leu Leu Leu Leu
 1 5 10 15
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 Leu Ser Leu Ala Ser Asn Val Ser Gly Leu Gln Cys Asn Ala Ser Val
 35 40 45
 Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser Pro Ala Gly Gln Leu Val
 50 55 60
 Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly Val Arg Tyr Asn Thr Thr
 65 70 75 80
 Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn Gly Ser Trp Ala Ala Arg
 85 90 95
 Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu Asn Glu Glu Lys Lys Ser
 100 105 110
 Lys Val His Tyr His Ile Ala Val Ile Ile Asn Tyr Leu Gly His Cys
 115 120 125
 Ile Ser Leu Val Ala Leu Leu Val Ala Phe Val Leu Phe Leu Arg Leu
 130 135 140
 Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile His Trp Asn Leu Ile Ser
 145 150 155 160
 Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe Val Val Gln Leu Thr Val
 165 170 175
 Ser Pro Glu Val His Gln Ser Asn Val Ala Trp Cys Arg Leu Val Thr
 180 185 190
 Ala Ala Tyr Asn Tyr Phe His Val Thr Asn Phe Phe Trp Met Phe Gly
 195 200 205
 Glu Gly Cys Tyr Leu His Thr Ala Ile Val Leu Thr Tyr Ser Thr Asp
 210 215 220
 Arg Leu Arg Lys Trp Met Phe Val Cys Ile Gly Trp Gly Val Pro Phe

225 230 235 240
 Pro Ile Ile Val Ala Trp Ala Ile Gly Lys Leu Tyr Tyr Asp Asn Glu
 245 250 255
 Lys Cys Trp Phe Gly Lys Arg Pro Gly Val Tyr Thr Asp Tyr Ile Tyr
 260 265 270
 Gln Gly Pro Met Ile Leu Val Leu Ile Asn Phe Ile Phe Leu Phe
 275 280 285
 Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser
 290 295 300
 Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu
 305 310 315 320
 Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu
 325 330 335
 Asp Glu Val Ser Arg Val Val Phe Ile Tyr Phe Asn Ser Phe Leu Glu
 340 345 350
 Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr Cys Phe Leu Asn Ser
 355 360 365
 Glu Val Arg Ser Ala Ile Arg Lys Arg Trp Arg Arg Trp Gln Asp Lys
 370 375 380
 His Ser Ile Arg Ala Arg Val Ala Arg Ala Met Ser Ile Pro Thr Ser
 385 390 395 400
 Pro Thr Arg Val Ser Phe His Ser Ile Lys Gln Ser Thr Ala Val
 405 410 415

<210> 14

<211> 1582

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (82)...(1413)

<223> CRF-R splice-variant insert fragment inserted

between nucleotides 516-517 of SEQ ID NO:1.

/note= "This sequence is contained in clone

"CRF-R2".

<400> 14

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ggtagccgag cgagcccgag g atg gga ggg cac ccg cag ctc cgt ctc gtc 111

Met Gly Gly His Pro Gln Leu Arg Leu Val

1 5 10

aag gcc ctt ctc ctt ctg ggg ctg aac ccc gtc tct gcc tcc ctc cag 159

Lys Ala Leu Leu Leu Leu Gly Leu Asn Pro Val Ser Ala Ser Leu Gln

15

20

25

gac cag cac tgc gag agc ctg tcc ctg gcc agc aac atc tca gga ctg 207
 Asp Gln His Cys Glu Ser Leu Ser Leu Ala Ser Asn Ile Ser Gly Leu
 30 35 40

cag tgc aac gca tcc gtg gac ctc att ggc acc tgc tgg ccc cgc agc 255
 Gln Cys Asn Ala Ser Val Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser
 45 50 55

cct gcg ggg cag cta gtg gtt cgg ccc tgc cct gcc ttt ttc tat ggt 303
 Pro Ala Gly Gln Leu Val Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly
 60 65 70

gtc cgc tac aat acc aca aac aat ggc tac cgg gag tgc ctg gcc aat 351
 Val Arg Tyr Asn Thr Thr Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn
 75 80 85 90

ggc agc tgg gcc gcc cgc gtg aat tac tcc gag tgc cag gag atc ctc 399
 Gly Ser Trp Ala Ala Arg Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu
 95 100 105

aat gag gag aaa aaa agc aag gtg cac tac cat gtc gca gtc atc atc 447
 Asn Glu Glu Lys Lys Ser Lys Val His Tyr His Val Ala Val Ile Ile
 110 115 120

aac tac ctg ggc cac tgt atc tcc ctg gtg gcc ctc ctg gtg gcc ttt 495
 Asn Tyr Leu Gly His Cys Ile Ser Leu Val Ala Leu Leu Val Ala Phe
 125 130 135

gtc ctc ttt ctg cgg ctc agg cca ggc tgc acc cat tgg ggt gac cag 543
 Val Leu Phe Leu Arg Leu Arg Pro Gly Cys Thr His Trp Gly Asp Gln
 140 145 150

gca gat gga gcc ctg gag gtg ggg gct cca tgg agt ggt gcc cca ttt 591
 Ala Asp Gly Ala Leu Glu Val Gly Ala Pro Trp Ser Gly Ala Pro Phe
 155 160 165 170

cag gtt cga agg agc atc cgg tgc ctg cga aac atc atc cac tgg aac 639
 Gln Val Arg Arg Ser Ile Arg Cys Leu Arg Asn Ile Ile His Trp Asn
 175 180 185

ctc atc tcc gcc ttc atc ctg cgc aac gcc acc tgg ttc gtg gtc cag 687
 Leu Ile Ser Ala Phe Ile Leu Arg Asn Ala Thr Trp Phe Val Val Gln
 190 195 200

cta acc atg agc ccc gag gtc cac cag agc aac gtg ggc tgg tgc agg 735
 Leu Thr Met Ser Pro Glu Val His Gln Ser Asn Val Gly Trp Cys Arg
 205 210 215

tig gtg aca gcc gcc tac aac tac ttc cat gtg acc aac ttc ttc tgg 783
 Leu Val Thr Ala Ala Tyr Asn Tyr Phe His Val Thr Asn Phe Phe Trp
 220 225 230

atg ttc ggc gag ggc tgc tac ctg cac aca gcc atc gtg ctc acc tac 831
 Met Phe Gly Glu Gly Cys Tyr Leu His Thr Ala Ile Val Leu Thr Tyr
 235 240 245 250

tcc act gac cgg ctg cgc aaa tgg atg ttc atc tgc att ggc tgg ggt 879
 Ser Thr Asp Arg Leu Arg Lys Trp Met Phe Ile Cys Ile Gly Trp Gly
 255 260 265

gtg ccc ttc ccc atc att gtg gcc tgg gcc att ggg aag ctg tac tac 927
 Val Pro Phe Pro Ile Ile Val Ala Trp Ala Ile Gly Lys Leu Tyr Tyr
 270 275 280

gac aat gag aag tgc tgg ttt ggc aaa agg cct ggg gtg tac acc gac 975
 Asp Asn Glu Lys Cys Trp Phe Gly Lys Arg Pro Gly Val Tyr Thr Asp
 285 290 295

tac atc tac cag ggc ccc atg atc ctg gtc ctg ctg atc aat ttc atc 1023
 Tyr Ile Tyr Gln Gly Pro Met Ile Leu Val Leu Leu Ile Asn Phe Ile
 300 305 310

ttc ctt ttc aac atc gtc cgc atc ctc atg acc aag ctc cgg gca tcc 1071
 Phe Leu Phe Asn Ile Val Arg Ile Leu Met Thr Lys Leu Arg Ala Ser
 315 320 325 330

acc acg tct gag acc att cag tac agg aag gct gtg aaa gcc act ctg 1119
 Thr Thr Ser Glu Thr Ile Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu
 335 340 345

gtg ctg ctg ccc ctc ctg ggc atc acc tac atg ctg ttc ttc gtc aat 1167
 Val Leu Leu Pro Leu Leu Gly Ile Thr Tyr Met Leu Phe Phe Val Asn
 350 355 360

ccc ggg gag gat gag gtc tcc cgg gtc gtc ttc atc tac ttc aac tcc 1215
 Pro Gly Glu Asp Glu Val Ser Arg Val Val Phe Ile Tyr Phe Asn Ser
 365 370 375

ttc ctg gaa tcc ttc cag ggc ttc ttt gtg tct gtg ttc tac tgt ttc 1263
 Phe Leu Glu Ser Phe Gln Gly Phe Phe Val Ser Val Phe Tyr Cys Phe
 380 385 390

ctc aat agt gag gtc cgt tct gcc atc cgg aag agg tgg cac cgg tgg 1311
 Leu Asn Ser Glu Val Arg Ser Ala Ile Arg Lys Arg Trp His Arg Trp
 395 400 405 410

cag gac aag cac tcg atc cgt gcc cga gtg gcc cgt gcc atg tcc atc 1359
 Gln Asp Lys His Ser Ile Arg Ala Arg Val Ala Arg Ala Met Ser Ile
 415 420 425

ccc acc tcc cca acc cgt gtc agc ttt cac agc atc aag cag tcc aca 1407
 Pro Thr Ser Pro Thr Arg Val Ser Phe His Ser Ile Lys Gln Ser Thr
 430 435 440

gca gtc tgagctggca ggtcatggag cagcccccaa agagctgtgg ctggggggat 1463
 Ala Val

gacggccagg ctccctgacc accctgectg tggaggtgac ctgttaggtc tcatgccac 1523
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<210> 15

<211> 444

<212> PRT

<213> Homo sapiens

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Leu Ser Leu Ala Ser Asn Ile Ser Gly Leu Gln Cys Asn Ala Ser Val

35 40 45

Asp Leu Ile Gly Thr Cys Trp Pro Arg Ser Pro Ala Gly Gln Leu Val

50 55 60

Val Arg Pro Cys Pro Ala Phe Phe Tyr Gly Val Arg Tyr Asn Thr Thr

65 70 75 80

Asn Asn Gly Tyr Arg Glu Cys Leu Ala Asn Gly Ser Trp Ala Ala Arg

85 90 95

Val Asn Tyr Ser Glu Cys Gln Glu Ile Leu Asn Glu Glu Lys Lys Ser

100 105 110

Lys Val His Tyr His Val Ala Val Ile Ile Asn Tyr Leu Gly His Cys

115 120 125

Ile Ser Leu Val Ala Leu Leu Val Ala Phe Val Leu Phe Leu Arg Leu
 130 135 140
 Arg Pro Gly Cys Thr His Trp Gly Asp Gln Ala Asp Gly Ala Leu Glu
 145 150 155 160
 Val Gly Ala Pro Trp Ser Gly Ala Pro Phe Gln Val Arg Arg Ser Ile
 165 170 175
 Arg Cys Leu Arg Asn Ile Ile His Trp Asn Leu Ile Ser Ala Phe Ile
 180 185 190
 Leu Arg Asn Ala Thr Trp Phe Val Val Gln Leu Thr Met Ser Pro Glu
 195 200 205
 Val His Gln Ser Asn Val Gly Trp Cys Arg Leu Val Thr Ala Ala Tyr
 210 215 220
 Asn Tyr Phe His Val Thr Asn Phe Phe Trp Met Phe Gly Glu Gly Cys
 225 230 235 240
 Tyr Leu His Thr Ala Ile Val Leu Thr Tyr Ser Thr Asp Arg Leu Arg
 245 250 255
 Lys Trp Met Phe Ile Cys Ile Gly Trp Gly Val Pro Phe Pro Ile Ile
 260 265 270
 Val Ala Trp Ala Ile Gly Lys Leu Tyr Tyr Asp Asn Glu Lys Cys Trp
 275 280 285
 Phe Gly Lys Arg Pro Gly Val Tyr Thr Asp Tyr Ile Tyr Gln Gly Pro
 290 295 300
 Met Ile Leu Val Leu Leu Ile Asn Phe Ile Phe Leu Phe Asn Ile Val
 305 310 315 320
 Arg Ile Leu Met Thr Lys Leu Arg Ala Ser Thr Thr Ser Glu Thr Ile
 325 330 335
 Gln Tyr Arg Lys Ala Val Lys Ala Thr Leu Val Leu Leu Pro Leu Leu
 340 345 350
 Gly Ile Thr Tyr Met Leu Phe Phe Val Asn Pro Gly Glu Asp Glu Val
 355 360 365
 Ser Arg Val Val Phe Ile Tyr Phe Asn Ser Phe Leu Glu Ser Phe Gln
 370 375 380
 Gly Phe Phe Val Ser Val Phe Tyr Cys Phe Leu Asn Ser Glu Val Arg
 385 390 395 400
 Ser Ala Ile Arg Lys Arg Trp His Arg Trp Gln Asp Lys His Ser Ile
 405 410 415
 Arg Ala Arg Val Ala Arg Ala Met Ser Ile Pro Thr Ser Pro Thr Arg
 420 425 430
 Val Ser Phe His Ser Ile Lys Gln Ser Thr Ala Val
 435 440